

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: SAGAWA, HIROAKI
UENO, HARUMI
OSHIMA, ATSUSHI
KATO, IKUNOSHIN

(ii) TITLE OF INVENTION: PLASMID

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: FALLS CHURCH
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22040-0747

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: WEINER, MARC S.
(B) REGISTRATION NUMBER: 32,181
(C) REFERENCE/DOCKET NUMBER: 1422-0319P

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "2=Val or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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FEB 20 2003

TECH CENTER 1600/2900

Met Xaa Pro Leu Asp Lys Asp Leu Gln Lys Ala Lys Ile Ser Ile Thr
 1 5 10 15
 Asp Phe Phe Glu Ile Thr Asn Arg Val Leu Asp Tyr Phe Pro Asn Val
 20 25 30
 Ile Asn Asn Thr Val Glu Lys Gly Asp Tyr Leu Ile Ser Ser Ser Asn
 35 40 45
 Ile Ala Gly Thr Ile Lys Phe Leu Arg Pro Ile Asn Arg Lys Leu Phe
 50 55 60
 Ile Gln Glu Lys Lys Val Phe Asn Asp Tyr Phe Gln Lys Leu Ile Ile
 65 70 75 80
 Val Phe Glu Asn Ile Arg Asn Lys Lys Thr Val Thr Glu Glu Asp Lys
 85 90 95
 Ile Ile Ile Asp Arg Val Ile Tyr Thr Ile Gln Gln Ser Ile Gly Ile
 100 105 110
 Gly Leu Asp Leu Met Val Asn Gln Asn Ser Ala Arg Lys His Val Gly
 115 120 125
 Asn Arg Phe Glu Glu Leu Ile Arg Val Ile Phe Thr Glu Ile Ser Val
 130 135 140
 Ser Asn Lys Arg Thr Val Leu Gln Ile Pro Tyr Glu Thr Asp Glu Gly
 145 150 155 160
 Gln Lys Ile Tyr Lys Cys Glu Asn Asp Leu Ile Ile Ser Pro Phe Glu
 165 170 175
 Asn Val Glu Ser Thr Asn Lys His Leu Asp Glu Asn Glu Ile Val Val
 180 185 190
 Ser Ile Lys Thr Thr Ser Lys Asp Arg Met Gly Lys Met Phe Ile Asp
 195 200 205
 Lys Ile Leu Leu Glu Arg Phe Val Lys His Pro Gln Lys Val Ile Gly
 210 215 220
 Ile Phe Leu Asn Asp Val Gln Arg Lys Glu Asp Asn Asn Ile Ser Phe
 225 230 235 240
 Thr Leu Val Ser Gly Leu Phe Met Val Tyr Thr Lys Phe Leu Thr Thr
 245 250 255
 Leu Glu Gly Ile Tyr Tyr Leu Asp Pro Pro Pro Asn Ala Leu Lys Leu
 260 265 270
 Pro Tyr Ser Asn His Met Lys Arg Phe Ser Asp Leu Ile Thr Glu Asp
 275 280 285
 Leu Glu Lys Leu Phe Ser Ser
 290 295

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 885 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGSTACCAC TGGATAAAGA TTTACAAAAA GCAAAGATTT CAATTACTGA TTTTTTTGAA	60
ATTACAAATA GAGTTTTAGA TTATTTCCTC AATGTAATCA ATAATACAGT TGAAAAAGGA	120
GATTATTTAA TATCCTCATC AAATATTGCT GGAACAATAA AATTCCTAAG ACCAATCAAT	180
AGAAAGTTAT TTATTCAGGA AAAAAAAGTT TTCAATGATT ATTTTCAAAA ACTGATTATA	240
GTTCCTTGAAA ATATAAGGAA CAAAAAACT GTAACAGAGG AAGATAAAAT TATTATTGAT	300
AGGGTAATTT ACACAATACA GCAATCTATT GGAATTGGTT TAGATTTAAT GGTTAATCAA	360
AATAGTGCTA GAAAGCACGT TGGTAACCGA TTTGAAGAAT TAATTAGAGT CATTTTACAA	420
GAAATATCAG TATCGAATAA AAGAACTGTA TTACAAATTC CATATGAAAC TGATGAAGGA	480
CAGAAAATTT ACAAATGCGA GAATGACCTC ATTATTCTC CTTTTGAAAA TGTAGAATCT	540
ACAAACAAAC ATCTAGATGA AAATGAGATT GTTGTTTCAA TAAAGACAAC ATCAAAAGAT	600
AGGATGGGAA AAATGTTTAT AGATAAAATT TTAAGTGAAA GGTTCGTAA ACACCTCAA	660
AAAGTTATAG GGATTTTCCT CAATGATGTA CAAAGAAAAG AAGACAACAA TATCAGCTTT	720
ACACTTGTTT CAGGATTATT TATGGTGTAT ACTAAATTCT TAACTACTCT TGAAGGGATC	780
TATTATTTAG ATCCACCACC TAATGCATTG AACTACCAT ATTCTAATCA TATGAAAAGA	840
TTTTCAGATT TAATTACAGA AGACCTTGAA AAATTATTCT CCTCT	885

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TATGGATATG TTCATAAACA CGCATGTAGG CAGATAGATC TTTGGTTGTG AATCGCAACC	60
AGTGGCCTTA TGGCAGGAGC CGCGGATCAC CTACCATCCC TAATGACCTG CAGGCATGCA	120

AGCTTGCATG CCTGCAGGTC ATTAGGTACG GCAGGTGTGC TCGAGGCGAA GGAGTGCCTG 180
 CATGCGTTTC TCCTGGCTT TTTCTCTG GGACA 215

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TATGTCCCAG AGGAAAAAAG CCAAGGAGAA ACGCATGCAG GCACTCCTTC GCCTCGAGCA 60
 CACCTGCCGT ACCTAATGAC CTGCAGGCAT GCAAGCTTGC ATGCCTGCAG GTCATTAGGG 120
 ATGGTAGGTG ATCCGCGGCT CCTGCCATAA GGCCACTGGT TCGGATTAC AACC AAAGAT 180
 CTATCTGCCT ACATGCGTGT TTATGAACAT ATCCA 215

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGATCTAGAG CAAACAAAAA AACCACCG 28

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTCTAGATC CCAGAGGAAA AAAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCGAGATTT AGGTGACACT ATAGAATACG GAATTGTGAG CGGATAACAA TTCCAAGCTT

60

CACAGGAAAC AGACCATGGC TTAAGTAACT AGTGAATTCG

100

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGAATTCCT AGTTACTTAA GCCATGGTCT GTTTCCTGTG AAGCTTGGAA TTGTTATCCG

60

CTCACAATTC CGTATTCTAT AGTGTCACCT AAATCTCGAG

100

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATCCCATGG AACGCTACGA ATCTCTG

27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGCCATGG TTATTTTGA CACCAGACC

29

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAACTGAAT CCATGGGTTC TCACCG

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TACTCAGTAG CCATGGCTCT CATAGACCG

29

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Asn	Glu	Ile	Ala	Phe	Asp	Asn	Tyr	Ser	Tyr	Ile	Pro	Lys	Leu	Lys
1				5					10					15	
Leu	Tyr	Ser	Glu	Ile	Glu	Leu	Lys	Pro	Phe	Phe	Ile	Ser	Lys	Asn	Gly
			20					25					30		
Ser	Leu	Phe	Asn	Val	Asp	Ala	Ile	Asp	Phe	Leu	Arg	Lys	Leu	Glu	Ser
		35					40					45			
Asn	Ser	Val	Asp	Leu	Ile	Phe	Ala	Asp	Pro	Pro	Tyr	Asn	Ile	Lys	Lys
		50				55					60				
Ala	Glu	Trp	Asp	Ile	Phe	Ser	Ser	Gln	Asn	Glu	Tyr	Leu	Glu	Trp	Ser
65				70						75				80	
Lys	Glu	Trp	Ile	Met	Glu	Ala	His	Arg	Val	Leu	Lys	Asp	Asn	Gly	Ser
			85					90						95	
Leu	Tyr	Val	Cys	Gly	Phe	Ser	Glu	Ile	Leu	Ala	Asp	Ile	Lys	Phe	Ile
			100					105					110		
Thr	Ser	Lys	Tyr	Phe	His	Ser	Cys	Lys	Trp	Leu	Ile	Trp	Phe	Tyr	Arg
		115					120					125			
Asn	Lys	Ala	Asn	Leu	Gly	Lys	Asp	Trp	Gly	Arg	Ser	His	Glu	Ser	Ile
		130				135					140				
Leu	Leu	Leu	Arg	Lys	Ser	Lys	Asn	Phe	Ile	Phe	Asn	Ile	Asp	Glu	Ala
145				150						155				160	
Arg	Ile	Pro	Tyr	Asn	Glu	His	Thr	Val	Lys	Tyr	Pro	Gln	Arg	Thr	Gln
			165						170					175	
Ala	Glu	Ser	Ser	Gln	Tyr	Ser	Asn	Ser	Lys	Lys	Gln	Tyr	Ile	Trp	Glu
			180					185					190		
Pro	Asn	Pro	Leu	Gly	Ala	Lys	Pro	Lys	Asp	Val	Leu	Glu	Ile	Pro	Thr
		195				200						205			
Ile	Ser	Asn	Gly	Ser	Trp	Glu	Arg	Ser	Ile	His	Pro	Thr	Gln	Lys	Pro
		210				215					220				
Val	Glu	Leu	Leu	Lys	Lys	Ile	Ile	Leu	Ser	Ser	Ser	Asn	Lys	Asp	Ser
225				230						235				240	
Leu	Ile	Leu	Asp	Pro	Phe	Gly	Gly	Ser	Gly	Thr	Thr	Tyr	Ala	Val	Ala
			245						250					255	
Glu	Ala	Phe	Gly	Arg	Lys	Trp	Ile	Gly	Thr	Glu	Leu	Asp	Lys	Asn	Tyr
			260					265					270		
Cys	Leu	Glu	Ile	Gln	Lys	Arg	Leu	Lys	Asp	Glu	Ser	Met	Ile	Asn	Arg

Ile Phe Ser Gly Asp Asp Asp Ser Asn Ser Gln Asn Arg Arg Lys Lys
 290 295 300
 Leu Arg Gly Glu
 305

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 924 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAATGAAA TAGCGTTTGA TAATTACAGT TATATACCAA AATTAAAACT TTATTCGGAA 60
 ATCGAGCTTA AACCATTTTT TATTTCAAAA AACGGTTCAC TTTTCAATGT TGATGCTATT 120
 GATTTTTTAA GAAAATTAGA GAGTAATTCT GTGGATTAA TTTTGCAGA TCCACCTTAT 180
 AACATTAAAA AGGCAGAGTG GGATATTTTT TCTTCTCAA ATGAATATCT CGAATGGAGT 240
 AAAGAATGGA TAATGGAAGC TCATAGAGTT TTAAGAGATA ATGGCAGTTT ATATGTTTGT 300
 GGCTTTTCAG AAATTCTGGC AGACATAAAA TTTATCACTT CAAATATTT TCACAGTTGT 360
 AAATGGTTGA TTTGGTTCTA TAGAAACAAG GCAAATTTAG GTAAAGATTG GGGACGTTCA 420
 CACGAAAGTA TACTGTTATT AAGAAAATCT AAAAATTTTA TTTTAATAT TGATGAGGCA 480
 CGAATCCCGT ATAATGAGCA TACAGTTAAA TATCCACAAA GAACCCAGGC CGAATCTTCG 540
 CAATATTCTGA ACTCAAAAAA GCAATATATT TGGGAGCCAA ACCCATTAGG AGCTAAGCCA 600
 AAAGATGTTT TGGAGATTCC CACAATTCA AATGGTTCTT GGGAAAGAAG TATCACCCCT 660
 ACGCAAAAGC CAGTAGAATT GCTTAAAAAA ATAATTTTAT CTTTCATCTAA TAAAGATAGT 720
 TTAATTCTTG ATCCATTGG TGGTTCGGGA ACTACATATG CTGTTGCGGA AGCTTTTGGC 780
 AGAAAATGGA TTGGAACAGA GTTAGATAAA AATTATTGTC TGGAAATTCA AAAGCGATTG 840
 AAAGACGAAA GTATGATCAA CAGGATTTTT TCAGGCGATG ATGATTCAAA TTCTCAAAAT 900
 AGAAGAAAAA AATTAAGAGG AGAA 924

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGAGATTTA GGTGACACTA TAGAATACA

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGCTTGTATT CTATAGTGTC ACCTAAATC

29

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCGAGATTTA GGTGACACTA TAGAATACGG AATTGTGAGC GGATAACAAT TCCA

54

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCTTGGAAT TGTTATCCGC TCACAATTCC GTATTCTATA GTGTCACCTA AATC

54

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Leu	Pro	Leu	Asp	Lys	Asp	Leu	Gln	Lys	Ala	Lys	Ile	Ser	Ile	Thr
1				5				10						15	

Asp	Phe	Phe	Glu
			20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: primer_bind
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "6, 9, 12 = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGTTNCCNY TNGAYAARGA YYT

23

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: primer_bind
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "9 = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGGATTTC ARAARGCNAA RAT

23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TAAATCTAAA CCAATTCCAA TAGATTGCTG

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAAATCTAAA CCAATTCCAA TAGATTGCTG

30

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAACTGTATT ACAAATTCCA TATGAACTG

30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACAGAAAAT TTACAAATGC GAGAATGACC

30

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCATGGCACA CGTTTCAAAA AAGAAATCCT CGAAGTCAAA TATGATGAGA AAAACATCTC	60
AGACATCCTG CATATGACGG TGGATGAAGC ATTGGAATTT TTCTCGGAAA ATCACGAAGA	120
AAAAATTGTA ACCAAACTAA AACCTTTGCA GGACGTTGGT TTGGGTTATC TTCAGTTAGG	180
CCAGTCCTCC TCTACTCTTT CCGGCGGTGA AGCCCAAAGA GTGAAGCTCG CCTCTTTCCT	240
TGTGAAAGGT GTAACGACGG AAAAAACGTT ATTTGTTTTT GATGAACCAT CAACAGGATT	300
ACATTTCCAC GACATTCAAA AATTACTGAA ATCACTTCAG GCACTGATAG AATTAGGGCA	360
TTCGGTTGTA GTGATTGAGC ATCAGCCGGA TATTATCAAA TGCGCCGATT ACATCATCGA	420
TGTCGGACCC AATGCCGGA AATACGGTGG CGAAATTGTT TTCACAGGAA CTCCGGAAGA	480
TTTGGTAAAA GAGAAAAAGT CGTTTACAGG GAAGTATATT AAGGAGAAGT TAAAGTAATT	540
TATTTATATT TGAAGTTATG CTACCACTGG ATAAAGATTT ACAAAAAGCA AAGATTTCAA	600
TTACTGATTT TTTTGAAATT ACAAATAGAG TTTTAGATTA TTTCCCAAT GTAATCAATA	660
ATACAGTTGA AAAAGGAGAT TATTTAATAT CCTCATCAAA TATTGCTGGA ACAATAAAAT	720
TCCTAAGACC AATCAATAGA AAGTTATTTA TTCAGGAAAA AAAAGTTTTC AATGATTATT	780

TTCAAAACT GATTATAGTT TTTGAAAATA TAAGGAACAA AAAAAGTGTGTA ACAGAGGAAG	840
ATAAAATTAT TATTGATAGG GTAATTTACA CAATACAGCA ATCTATTGGA ATTGGTTTAG	900
ATTTAATGGT TAATCAAAAT AGTGCTAGAA AGCACGTTGG TAACCGATTT GAAGAATTAA	960
TTAGAGTCAT TTTTACAGAA ATATCAGTAT CGAATAAAAG AACTGTATTA CAAATTCCAT	1020
ATGAACTGA TGAAGGACAG AAAATTTACA AATGCGAGAA TGACCTCATT ATTTCTCCTT	1080
TTGAAAATGT AGAATCTACA AACAAACATC TAGATGAAAA TGAGATTGTT GTTCAATAA	1140
AGACAACATC AAAAGATAGG ATGGGAAAAA TGTATATAGA TAAATTTTA CTTGAAAGGT	1200
TTGTTAAACA CCTCAAAAA GTTATAGGGA TTTTCCTCAA TGATGTACAA AGAAAAGAAG	1260
ACAACAATAT CAGCTTTACA CTTGTTTCAG GATTATTTAT GGTGTATACT AAATTCTTAA	1320
CTACTCTTGA AGGGATCTAT TATTTAGATC CACCACCTAA TGCATTGAAA CTACCATATT	1380
CTAATCATAT GAAAAGATTT TCAGATTTAA TTACAGAAGA CCTTGAAAAA TTATTCTCCT	1440
CTTAATTTTT TTCTTCTATT TTGAGAATTT GAATCATCAT CGCCTGAAAA AATCCTGTTG	1500
ATCATACTTT CGTCTTTCAA TCGCTTTTGA ATTCCAGAC AATAATTTTT ATCTAACTCT	1560
GTTCCAATCC ATTTTCTGCC AAAAGCTT	1588

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATATTTGAAG CCATGGTACC ACTGG

25

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGATCTGGTC ATCCCAAACA AAAATCTTTC GGTTTACGAA GATGCAGTCG CTCCTGGAA	60
AGGCGAAAGT ATGAGCGAAT GGAAAAAGGA ATTCATCAAA AAAGCCAAAG ATTTCCCAAT	120
TCACAAGCCT TATCATCAAC TCACAAAAGA GCAGAAACAG TTCCTTTGGA AAGGCGATAA	180
AACCAGAAGT TTCCAAGTA TTGATAATTT TTTCAAAATG CTTGAAGAGA ATCTTTACAA	240
GATCCAATAC CGCGTAATGC TTTTCGCGCTA TCGTGGGAAA ACACTTTGCC CCGATTGCGA	300
AGGATTACGA TTGCGGGAAG AAACAAGCTG GGTGAAGATT GACGGACACA ACATTCAGTC	360
TTTGATTGAA TTACCTTTGG ATGAACTCCT GCCATTGATC AAAAGCTTAA AACTGAACGT	420
CCACGACAGA GAAATTGCCA AACGCCTGAC TTACGAAATC GAAACGAGAT TAGAATTCTT	480
GACGAAAGTC GGCCTTGGAT ATCTGACTTT GAACCGAACA TCCAACACGC TTTCCGAGG	540
AGAAAGCCAG AGAATCAATC TGGCGACAGC TTGGGAAGTT CGCTGGTTGG TTCTATTTAT	600
ATTTTGATG AGCCGAGCAT TGGTCTGCAT TCCC GCGATA CAGAAAATCT GATTGGTGTC	660
CTCAAACAAC TCCGCGATTT GGGAANTACC GTGATTGTTG TAGAACACGA CGAAGATGTG	720
ATGCTTGCGG CAGNTTACAT TATAGATATT GGCCCNAG CGGGCTACCT TGGTGGCGAT	780
CTTGTTTTCA GCGNGGATTA TAAAGAGATG CTGAAGTNTN ATACTTTAAC CGCAAAATAC	840
CTGAATGGCG AACTGAAAAT AGAAGTTCCT GAAAAACGAA GAAAACCGAA GGAATTCATC	900
GCAATAAAAG GTGCCCAGCA GAATAATTTA AAAAATATTG ACGTTGATGT TCCGTTAGAA	960
TGTCTGACAG TTATCACAGG CGTTTCTGGA AGCGGAAAT CCACTTTGAT GAAGGAAGTG	1020
ATGACCAATG CCATCCAGAT CCAACTGGGA ATGGGCGGCA AAAAAGCCGA TTACGATTCTG	1080
GTGGAATTCC CGAAAAAGCT GATCCAGAAT ATCGAACTGA TTGACCAGAA CCAATCGGG	1140
AAATCGTCCC GCTCCAACCC CGTGACTTAT CTGAAAGCTT ACGACGATAT CCGGGATCTT	1200
TTTGCGAAAC AAAAATCCGC AAAAATCCAG GGTACAAAC CGAAGCATTT CTCCTTCAAT	1260
GTGGATGGCG GAAGATGTGA CGAGTGCAAA GGCGAAGGTA TCATTACCGT ATCAATGCAG	1320

TTTATGGCGG ACATCGAGCT GGAGTGTGAG CATTGCCATG GCACACGTTT CAAAAAAGAA	1380
ATCCTCGAAG TCAAAATATGA TGAGAAAAAC ATCTCAGACA TCCTGCATAT GACGGTGGAT	1440
GAAGCATTGG AATTTTCTC GGAAAATCAC GAAGAAAAAA TTGTAACCAA ACTAAAACCT	1500
TTGCAGGACG TTGGTTTGGG TTATCTTCAG TTAGGCCAGT CCTCCTCTAC TCTTCCGGC	1560
GGTGAAGCCC AAAGAGTGAA GCTCGCCTCT TTCCTTGTGA AAGGTGTAAC GACGGAAAAA	1620
ACGTTATTTG TTTTGTATGA ACCATCAACA GGATTACATT TCCACGACAT TCAAAAATTA	1680
CTGAAATCAC TTCAGGCACT GATAGAATTA GGCATTTCGG TTGTAGTGAT TGAGCATCAG	1740
CCGGATATTA TCAAAATGCGC CGATTACATC ATCGATGTCG GACCCAATGC CGGAAAATAC	1800
GGTGGCGAAA TTGTTTTCAC AGGAACTCCG GAAGATTGG TAAAAGAGAA AAAGTCGTTT	1860
ACAGGGAAGT ATATTAAGGA GAAGTTAAAG TAATTTATTT ATATTTGAAG TTATGCTACC	1920
ACTGGATAAA GATTTACAAA AAGCAAAGAT TTCAATTACT GATTTTTTTG AAATTACAAA	1980
TAGAGTTTTA GATTATTTCC CCAATGTAAT CAATAATACA GTTGAAAAAG GAGATTATTT	2040
AATATCCTCA TCAAAATATTG CTGGAACAAT AAAATTCCTA AGACCAATCA ATAGAAAGTT	2100
ATTTATTCAG GAAAAAAAAG TTTTCAATGA TTATTTTCAA AAAGTGATTA TAGTTTTTGA	2160
AAATATAAGG AACAAAAAAA CTGTAACAGA GGAAGATAAA ATTATTATTG ATAGGGTAAT	2220
TTACACAATA CAGCAATCTA TTGGAATTGG TTAGATTTA ATGGTTAATC AAAATAGTGC	2280
TAGAAAGCAC GTTGGTAACC GATTGAAGA ATTAATTAGA GTCATTTTTA CAGAAATATC	2340
AGTATCGAAT AAAAGAACTG TATTACAAAT TCCATATGAA ACTGATGAAG GACAGAAAAT	2400
TTACAAATGC GAGAATGACC TCATTATTTT TCCTTTTGAA AATGTAGAAT CTACAAACAA	2460
ACATCTAGAT GAAAATGAGA TTGTGTGTTT AATAAGACA ACATCAAAG ATAGGATGGG	2520
AAAAATGTTT ATAGATAAAA TTTTACTTGA AAGGTTTGTT AAACACCCTC AAAAAGTTAT	2580
AGGGATTTTC CTCAATGATG TACAAAGAAA AGAAGACAAC AATATCAGCT TTACACTTGT	2640
TTCAGGATTA TTTATGGTGT ATACTAAATT CTTAATACT CTTGAAGGGA TCTATTATTT	2700
AGATCCACCA CCTAATGCAT TGAACTACC ATATTCTAAT CATATGAAAA GATTTTCAGA	2760
TTTAATTACA GAAGACCTTG AAAAATTATT CTCCTCTTAA TTTTTTCTT CTATTTTGAG	2820
AATTTGAATC ATCATCGCCT GAAAAAATCC TGTGATCAT ACTTTCGTCT TTCAATCGCT	2880
TTTGAATTC CAGACAATAA TTTTATCTA ACTCTGTTCC AATCCATTTT CTGCCAAAAG	2940
CTTCCGCAAC AGCATATGTA GTTCCCGAAC CACCAAATGG ATCAAGAATT AAATATCTT	3000
TATTAGATGA AGATAAAATT ATTTTTTAA GCAATTCTAC TGGCTTTTGC GTAGGGTGAA	3060
TACTTCTTTC CCAAGAACCA TTTGAAATTG TGGGAATCTC CAAAACATCT TTTGGCTTAG	3120

CTCCTAATGG GTTTGGCTCC CAAATATATT GCTTTTTTGA GTTCGAATAT TGCGAAGATT	3180
CGGCCTGGGT TCTTTGTGGA TATTTAACTG TATGCTCATT ATACGGGATT CGTGCCTCAT	3240
CAATATTAAA AATAAAATTT TTAGATTTTC TTAATAACAG TATACTTTTCG TGTGAACGTC	3300
CCCAATCTTT ACCTAAATTT GCCTTGTTTC TATAGAACCA AATCAACCAT TTACAACTGT	3360
GAAAATATTT TGAAGTGATA AATTTTATGT CTGCCAGAAT TTCTGAAAAG CCACAAACAT	3420
ATAAACTGCC ATTATCTTTT AAAACTCTAT GAGCTTCCAT TATCCATTCT TTAATCCATT	3480
CGAGATATTC ATTTTGAGAA GAAAAAATAT CCCACTCTGC CTTTTTAATG TTATAAGGTG	3540
GATCTGCAAA AATTAAATCC ACAGAATTAC TCTCTAATTT TCTTAAAAAA TCAATAGCAT	3600
CAACATTGAA AAGTGAACCG TTTTTTGAAA TAAAAAATGG TTTAAGCTCG ATTTCCGAAT	3660
AAAGTTTTAA TTTTGGTATA TAACTGTAAT TATCAAACGC TATTTTCATT CAAATGAAT	3720
CAATCTGCTG TTGTGTATAA ACCCTGTAAT TATTAATAGG ATGTCTTAAA CTTTTGAATT	3780
TTCCAGAATT ATCCCATCTT CCTTAATGTC TCAGAGTTAA CATCTAATAA TTTGCGCGCT	3840
TCTTTTATTG ATAAATAATC ATCCATATCT TACACAACAT TACACAAGTT TATACAGCAA	3900
ATATAAATAT TTTTATACA TTGTAAAAAT TTTATTACT TTTATTTTGT TCAATTGTCT	3960
CAATAAATAG TTAATCGAAA TACATTTTGA ATATGATAAA ATTGACTCCA ACAAATCTAA	4020
CACAATGACA TTAAACCAA TAAAAACGGA AGAAGATTAC AATCAGGTTT TAGAAAGACT	4080
TTCACAAATT TTCGACGCTA AACCAAATAC CAAAGATGGA GATGAATTGG GAAATCTTGG	4140
GAATTC	4146

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATTTAGGTGA CACTATAGAA TAC

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAGCTCGAGT CTGATGACGA AGCTTGACTG ACTGAGATCA GCTTGCAAC

49

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGAGATTT AGGTGACACT ATAGAATACA AGCTT

35

(2) INFORMATION FOR SEQ ID NO:33:

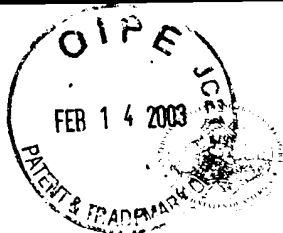
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCGAGATTT AGGTGACACT ATAGAATACG GAATTGTGAG CGGATAACAA TTCCAAGCTT

60



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Please find below and or attached an Office communication concerning this application or proceeding.

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